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OM protein - protein search, using sw model

Run on: July 1, 2003, 17:42:19 ; Search time 23 seconds

(Without alignments)
732.147 Million cell updates/sec

Title: US-09-782-587b-1

Perfect score: 2187
Sequence: 1 ANAFKXXLRPGSLRXCKXX.....LQKLRSEPRGVLLRAPFP 406

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query Match	Length	ID	Description
1	2167	99.1	466	FA7_HUMAN	P08709 homo sapien
2	1634.5	74.7	444	FA7_RABIT	P98139 oryctolagus
3	1567.5	71.7	446	FA7_MOUSE	P70375 bos taurus
4	1566	71.6	407	FA7_BOVIN	P22457 bos taurus
5	858.5	39.3	475	FA10_CHICK	P25155 gallus gall
6	858.5	39.3	488	FA10_HUMAN	P00742 homo sapien
7	850.5	38.9	416	FA9_BOVIN	P00740 homo sapien
8	849	38.8	461	FA9_HUMAN	P00740 homo sapien
9	843.5	38.6	490	FA10_RABIT	P16294 mus musculu
10	843	38.5	492	FA10_BOVIN	P16294 mus musculu
11	824	37.7	459	FA9_MOUSE	P19540 canis famli
12	821	37.5	452	FA9_CANFA	P19540 canis famli
13	786.5	36.0	459	PRIC_PIG	P31394 ratius norv
14	775	35.4	461	PRIC_PIG	P31394 ratius norv
15	769	35.2	461	PRIC_MOUSE	P31394 ratius norv
16	760	34.8	376	FA10_TROCA	P81428 tropidechis
17	749	34.2	456	PRIC_BOVIN	P00745 bos taurus
18	743	34.0	458	PRIC_RABIT	P00745 bos taurus
19	726	33.2	461	PRIC_HUMAN	P04070 homo sapien
20	519.5	23.8	275	FA9_RABIT	P16292 oryctolagus
21	515.5	23.6	281	FA9_RAT	P16292 oryctolagus
22	513.5	23.5	271	FA9_PIG	P16293 sus scrofa
23	511	23.4	285	FA9_CAVPO	P16291 cavia porce
24	509.5	23.3	274	FA9_SHEEP	P16291 cavia porce
25	473	21.6	638	KAL_MOUSE	P26362 mus musculu
26	463.5	21.2	653	HGR_MOUSE	P26362 mus musculu
27	461.5	21.1	638	KAL_RAT	P14772 ratius norv
28	459.5	21.0	638	KAL_HUMAN	P03952 homo sapien
29	444	20.4	343	PSS8_HUMAN	P16651 homo sapien
30	444	20.3	625	FA11_HUMAN	P03951 homo sapien
31	443.5	20.3	342	PSS8_RAT	P03951 homo sapien
32	443.5	20.3	622	THRB_HUMAN	P00734 ratius norv
33	442	20.2	342	PSS8_MOUSE	P00734 ratius norv

ALIGNMENTS

RESULT 1	FA7_HUMAN	STANDARD;	PRT;	466 AA.	
AC	P08709: 014339;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).				
DE	conversion accelerator) (Eptacog alfa).				
GN	F7.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RC	MEDLINE=86205965; PubMed=3486420;				
RA	Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,				
RA	Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kirachi K.,				
RA	David E.W.;				
RT	Characterization of a cDNA coding for human factor VII.;				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=87260948; PubMed=3037537;				
RA	O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,				
RA	Hagen F.S., Murray M.J.;				
RT	Nucleotide sequence of the gene coding for human factor VII, a				
RT	vitamin K-dependent protein participating in blood coagulation.;				
RL	Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.				
RA	Rieder M.J., Atmel T.Z., Carrington D.P., Chung M.W., Lee K.L.,				
RA	Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;				
RT	Submitted (JAN-2002) to the EMBL/GenBank/DBS databases.				
RL	[4]				
RP	SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.				
RA	MEDLINE=89088153; PubMed=3264725;				
RA	Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,				
RT	Pedersen A.H., Hedner U.;				
RT	Amino acid sequence and posttranslational modifications of human				
RT	factor VIIa from plasma and transfected baby hamster kidney cells.;				
RL	Biochemistry 27:7785-7793(1988).				
RN	[5]				
RP	CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.				
RA	MEDLINE=91250411; PubMed=1904059;				
RA	Bjorn S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,				
RT	Komiyama Y., Pedersen A.H., Kistiel W.;				
RT	Human plasma and recombinant factor VII. Characterization of O-				
RT	glycosylations at serine residues 52 and 60 and effects of site-				
RT	directed mutagenesis of serine 52 to alanine.;				
RL	J. Biol. Chem. 266:11051-11057(1991).				
RN	[6]				
RP	STRUCTURE OF CARBOHYDRATE ON SER-112.				
RA	MEDLINE=90062160; PubMed=2511201;				

34	439.5	20.1	655	1	HQFA_HUMAN	004756 homo sapien
35	439.5	20.1	1069	1	ENTK_MOUSE	P97435 mus musculu
36	428.5	19.6	625	1	THRB_BOVIN	P00735 bos taurus
37	428	19.6	1035	1	ENTK_BOVIN	P98072 bos taurus
38	426.5	19.5	246	1	TRYL_RAT	P19221 ratius norv
39	425.5	19.5	618	1	THRB_MOUSE	P00764 mus musculu
40	423	19.3	229	1	TRYP_SODAC	P00764 mus musculu
41	423	19.3	492	1	TMS2_HUMAN	015393 homo sapien
42	421	19.3	617	1	THRB_RAT	P18282 ratius norv
43	420.5	19.2	247	1	TRJ3_RAT	P08426 ratius norv
44	419.5	19.2	416	1	HEPS_MOUSE	035453 mus musculu
45	418	19.1	1019	1	ENTK_HUMAN	P98073 homo sapien

RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein 2 and bovine protein 2.";
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE-91344709; PubMed-2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein 2.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE-96175641; PubMed-8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE-99126538; PubMed-9925787;
 RA Zhang E., St Charles R., Tullinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPTI mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE-96367502; PubMed-9692950;
 RA Muranyi A., Finn B.E., Glibert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE-91300046; PubMed-2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE-92340074; PubMed-1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE-93372811; PubMed-8364544;
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE-94061028; PubMed-8242057;
 RA Takamiya O., Kembaiya O., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE-94264305; PubMed-8204879;
 RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.W., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE-95072589; PubMed-7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MET HIS-307.
 RX MEDLINE-95064662; PubMed-7974346;
 RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (C6C) for Arg(247) (CGC) in the
 RT catalytic domain.";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE-96247510; PubMed-8652821;
 RA Ardin A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS W-283, K-325, V-358, Q-364, E-402 AND Q-413.
 RX MEDLINE-97001216; PubMed-8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE-97037613; PubMed-8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zalzov R., Seligsohn U.;
 RT "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE-98112461; PubMed-9452082;
 RA Alshlawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN [22]
 RP FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC [23]
 RP CATALYTIC ACTIVITY: Hydrolyzes one Arg-1-Ile bond in factor X to
 CC form factor Xa.
 CC [24]
 RP SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC [25]
 RP ALTERNATIVE PRODUCTS: 2 isoforms: A (shown here) and B: are
 CC produced by alternative splicing.
 CC [26]
 RP TISSUE SPECIFICITY: PLASMA.
 CC [27]
 RP PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC [28]
 RP DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.
 CC [29]
 RP PHARMACEUTICAL: Available under the names Niasase or Novoseven
 CC (Novo Nordisk). Used for the treatment of bleeding episodes in

Query Match	99.1%	Score 2167	DB 1	Length 466
Best Local Similarity	97.5%	Pred. No. 9.6e-162		
Matches 396	Conservative 0	Mismatches 10	Indels 0	Gaps 0
QY	1	ANAFELXXRPSLSLKXKXKXQCSFFXAXRIFRDAXRTLFMTSYSDGOCASSPQONGS	60	
Db	61	ANAFLEELRPSLSRECKEBCQCSPEAEIRKDAERITLFMTSYSDGOCASSPQONGS	120	
QY	61	CKDQLOSTYFCFLPAFEGRCNETHKDDQLICVNGGCEQYCSDHGTGRSCRCHEGYSL	120	
Db	121	CKDQLOSTYFCFLPAFEGRCNETHKDDQLICVNGGCEQYCSDHGTGRSCRCHEGYSL	180	
QY	121	LADGVSCPTVEYPCGKPILEKRNASKPQGRIVGKXCPGCEQWVLLLYNGAQLCGG	180	
Db	181	LADGVSCPTVEYPCGKPILEKRNASKPQGRIVGKXCPGCEQWVLLLYNGAQLCGG	240	
QY	181	TLTNTIWWVSAHCFDKIKMNRNLIAVAGEHDLSEHDDQESRRVAGYIIPSTYPGTTN	240	
Db	241	TLTNTIWWVSAHCFDKIKMNRNLIAVAGEHDLSEHDDQESRRVAGYIIPSTYPGTTN	300	
QY	241	HDIALLLRHQVYLTIDHWVPLCLPEPRFSEETLAFVRSLSVSGMQLIDRQATALEMVL	300	
Db	301	HDIALLLRHQVYLTIDHWVPLCLPEPRFSEETLAFVRSLSVSGMQLIDRQATALEMVL	360	
QY	301	NVPLRLMTQDCLOQSRKVGDSNPINIEYFECACYSQGSNRKSGDGGGPHATYRGWYLTG	360	
Db	361	NVPLRLMTQDCLOQSRKVGDSNPINIEYFECACYSQGSNRKSGDGGGPHATYRGWYLTG	420	
QY	361	IVSGGCGCATVGHGCVYTRVSQYIEMLOKLMRSEPRPVLLRAEFP	406	
Db	421	IVSGGCGCATVGHGCVYTRVSQYIEMLOKLMRSEPRPVLLRAEFP	466	

RESULT 2

FA7_RABIT STANDARD: PRT: 444 AA.

AC P98139; P79224;

DT 01-FEB-1996 (Rel. 33, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).

DE F7.

GN

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RC MEDLINE=93190306; PubMed=80393365;

RX Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;

RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII."

RL Thromb. Res. Suppl. 69:231-238(1993).

RN [2]

RP REVISION TO 395.

RC TISSUE=Liver;

RC Ruiz S.R., Blajchman M.A., Clarke B.J.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC - FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).

CC - CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor xa.

CC - SUBUNIT: HEMERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).

CC - TISSUE SPECIFICITY: PLASMA.

CC	-I- PTM-THE VITAMIN K-DEPENDENT ENZYMIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
CC	-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC	-I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-stb.ch/announce/ or send an email to license@isb-stb.ch).
CC	-----
DR	EMBL; U72477; AAB37326.1; .
DR	HSPB; P08709; IFAK.
DR	MEROPS; S01.215; .
DR	InterPro: IPR0001152; Asx_hydroxyl.
DR	InterPro: IPR001314; Chymotrypsin.
DR	InterPro: IPR000561; EGF-like.
DR	InterPro: IPR000742; EGF_2.
DR	InterPro: IPR001881; EGF_Ca.
DR	InterPro: IPR002383; GLA_blood.
DR	InterPro: IPR001254; Ser_protase_Try.
DR	InterPro: IPR000294; VitK_dep_Gla.
DR	Pfam; PF00008; EGF_2.
DR	Pfam; PF00089; trypsin; 1.
DR	Pfam; PF00594; gla; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR00001; GLABLOOD.
DR	SMART; SM00179; EGF_CA; 1.
DR	SMART; SM00001; EGF_like; 1.
DR	SMART; SM00069; GLA; 1.
DR	SMART; SM00020; TRYD-spec; 1.
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS01186; EGF_2; 1.
DR	PROSITE; PS01187; EGF_CA; 1.
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR	PROSITE; PS50240; TRYPsin_DOM; 1.
DR	PROSITE; PS00134; TRYPsin_HIS; 1.
DR	PROSITE; PS00135; TRYPsin_SER; 1.
KW	Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasmn; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; Egg-like domain; Repeat; Signal; Hydroxylation.
KW	Egg-like domain; Repeat; Signal; Hydroxylation.
FT	SIGNAL 1 21 POTENTIAL.
FT	PROPEP 22 39 POTENTIAL.
FT	CHAIN 40 191 FACTOR VII LIGHT CHAIN.
FT	CHAIN 192 444 FACTOR VII HEAVY CHAIN.
FT	DOMAIN 45 74 GLA-RICH.
FT	DOMAIN 85 121 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN 126 167 EGF-LIKE 2.
FT	DOMAIN 192 444 SERINE PROTEASE.
FT	DOMAIN 191 192 CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN) (BY SIMILARITY).
FT	ACT_SITE 232 232 BY SIMILARITY.
FT	ACT_SITE 281 281 BY SIMILARITY.
FT	ACT_SITE 383 383 BY SIMILARITY.
FT	BINDING 377 377 SUBSTRATE (BY SIMILARITY).
FT	DISEUFID 56 61 BY SIMILARITY.
FT	DISEUFID 89 100 BY SIMILARITY.
FT	DISEUFID 94 109 BY SIMILARITY.
FT	DISEUFID 111 120 BY SIMILARITY.
FT	DISEUFID 130 141 BY SIMILARITY.
FT	DISEUFID 137 151 BY SIMILARITY.
FT	DISEUFID 153 166 BY SIMILARITY.
FT	DISEUFID 174 301 BY SIMILARITY.
FT	DISEUFID 198 203 BY SIMILARITY.
FT	DISEUFID 217 233 BY SIMILARITY.
FT	DISEUFID 349 368 BY SIMILARITY.
FT	DISEUFID 379 407 BY SIMILARITY.
FT	MOD_RES 45 45 GAMMA-CARBOXYGUTAMIC ACID.
FT	MOD_RES 46 46 GAMMA-CARBOXYGUTAMIC ACID.

RESULT 4	FFA7_BOVIN	STANDARD:	PRT:	407 AA.
ID	FA7_BOVIN			
AC	P22457:			
ADT	01-AUG-1991 (Rel. 19, Created)			
DDT	01-AUG-1991 (Rel. 19, Last sequence update)			
DDT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).			
GN	F7.			
OS	Bos taurus (Bovine).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OS	Bovidae; Bovinae; Bos.			
OS	NCBI_TaxID=9913;			
OS	[1]			
OS	SEQUENCE.			
OS	MEDLINE=89008362; PubMed=3049594;			
OS	Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.			

RA Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid
sequence.";
RL J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE-8921399; Pubmed-1149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RT Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
blood coagulation factors VII and IX";
RL J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52..
RX MEDLINE-91344709; Pubmed-2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
RT "A new trisaccharide sugar chain linked to a serine residue in the
first EGF-like domain of clotting factors VII and IX and protein Z.";
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RN -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-I-tile bond in factor X to
CC form factor xa.
CC -1- SUBUNIT: HEMERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PMN: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC PIR: A31979; A31979.
CC HSSP; P08709; IBF9.
DR MEROPS; S01_215; -.
DR InterPro: IPRO00152; Asx_hydroxyl.
DR InterPro: IPRO01314; Chymotrypsin.
DR InterPro: IPRO00561; EGF-like.
DR InterPro: IPRO00742; EGF-2.
DR InterPro: IPRO01861; EGF-Ca.
DR InterPro: IPRO01438; EGF_I1.
DR InterPro: IPRO02383; GfA_blood.
DR InterPro: IPRO01254; Ser.protease_Try.
DR InterPro: IPRO00294; VitK_dep_GLA.
DR Pfam; PR00008; EGF_2.
DR Pfam; PR00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF-2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLTION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HTS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
ET 153 407 FACTOR VII HEAVY CHAIN.
FT DOMAIN 6 35 GFA-RICH.
FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 87 128 EGF-LIKE 2.

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FT DOMAIN 153 407 SERINE PROTEASE.
FT SITE 152 153 CLEAVAGE (BY FACTOR XA, FACTOR XIII,
FT ACT_SITE 193 193 FACTOR IXA, OR THROMBIN).
FT ACT_SITE 242 242 BY SIMILARITY.
FT ACT_SITE 242 242 BY SIMILARITY.
FT BINDING 344 344 BY SIMILARITY.
FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.
FT DISULFID 72 81 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT DISULFID 98 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 135 262 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 178 194 BY SIMILARITY.
FT DISULFID 310 329 BY SIMILARITY.
FT DISULFID 340 368 BY SIMILARITY.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT CARBOHYD 52 52 O-LINKED (GLC. . .).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
FT SEQUENCE 407 AA; 703ELFED06367FE1D CRC64;

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Query Match 71.6%; Score 1566; DB 1; Length 407;
Best Local Similarity 69.6%; Pred. No. 5,7e-115;
Matches 275; Conservative 45; Mismatches 75; Indels 0; Gaps 0;

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OY 1 ANAFLXLRGSLRXKCKXKXCCSPXAXRATFKDAXRKLWISYSGDDCASSPCONGGS 60
DB 1 ANGFLLELPGLSLERECELECSFEENHELFERNERROWWSYNDDQCASSPCONGGS 60
OY 61 CKDOLSYICFCLPAFGRNCETHKIDOLICVNEGSCDEQSDHGTGRKSCHEGYSL 120
DB 61 CEQOLRBYICFCDFGFRNCERTDKOSQLCANDNGCEQYCGADPEAGNFCWCHESYAL 120
OY 121 LADGVSCTPVEYPCGKIPILERKRNASKPOGRIVGKVCPCGECPMQVLLVNGAOLCG 180
DB 121 QADGVSCAPVEYPCGKIPILERKRNASKPOGRIVGKVCPCGECPMQVLLVNGAOLCG 180
OY 181 TLINTIYVNSAACHCFDKIKKRNULIAVLEHDI;SEHDCDQSRRAVAVITIPSTYVPGTTN 240
DB 181 TLVGPVAVNSAACHCFERLRSRGNLIVLGEHDS;SRVGEQERRVAQIIVPKQYVPGQTD 240
OY 241 HDVALRLHOPVVLTDHVPVLC;PERFESERTLAFRELSVSGMQLDGALELMVL 300
DB 241 HDVALRLHOPVVLTDHVPVLC;PERFESERTLAFRELSVSGMQLDGALELMVL 300
OY 301 NVRRLMTQDLOQSRKVGDSPTITEYFACAGYSDGSDCKGSGGPHATYHGTWLTG 360
DB 301 LVRRLMTQDLOQSRKVGDSPTITEYFACAGYSDGSDCKGSGGPHATYHGTWLTG 360
OY 361 IVSMGGCATGVHFGYVTRYSQYIEMQIKMRSEP 395
DB 361 IVSMGGCATGVHFGYVTRYSQYIEMQIKMRSEP 395

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RESULT 5
FASTA_CHUNK STANDARD; PRT; 475 AA.
AC P25155;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
DE (Virus activating protease) (VAP).
GN Ex.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE=Chorioallantoic membrane;
RX MEDLINE=91257322; PubMed=2044767;
RA Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotch B.,
RA Ogawara T., Nagai Y.;
RT "Primary structure of the virus activating protease from chick
RT embryo. Its identity with the blood clotting factor Xa.";
RL FEBS Lett. 283:281-285(1991).
RN [2]
RP SEQUENCE OF 41-55 AND 241-261.
RC TISSUE=Allantoic fluid;
RX MEDLINE=91065352; PubMed=2174359;
RA Gotch B., Ogawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,
RA Nagai Y.;
RT "An endoprotease homologous to the blood clotting factor X as a
RT determinant of viral tropism in chick embryo.";
RL EMBO J. 9:4189-4195(1990).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,
CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC SAC.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Thr and then
CC Arg-I-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
CC -1- P.M: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -1- P.M: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; D00844; BAA00724.1; -
DR PIR; S15838; S15838.
DR HSSP; P00742; 1HCG.
DR
DR MEROPS; S01.216; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF_1like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitr_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

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DR PRINTS; PRO0010; EGFBLD.
 DR PRINTS; PRO0001; GLABLOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF-1; 1.
 DR PROSITE; PS01186; EGF-2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYP_SIN_DOM; 1.
 DR PROSITE; PS00135; TRYP_SIN_SER; 1.
 DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
 Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 Signal; Zymogen; EGF-like domain; Repeat.
 OR 30, OR 31 (POTENTIAL).
 FT PROPEP 1 20
 FT CHAIN 21 40
 FT CHAIN 41 180
 FT PROPEP 186 475
 FT CHAIN 186 475
 FT CHAIN 242 475
 FT DOMAIN 86 122
 FT DOMAIN 125 168
 FT DOMAIN 241 475
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 FT MOD_RES 65 65
 FT MOD_RES 66 66
 FT MOD_RES 69 69
 FT MOD_RES 72 72
 FT MOD_RES 79 79
 FT MOD_RES 103 103
 FT ACT_SITE 328 328
 FT ACT_SITE 328 328
 FT ACT_SITE 425 425
 FT DISULFID 90 101
 FT DISULFID 95 110
 FT DISULFID 112 121
 FT DISULFID 129 140
 FT DISULFID 136 152
 FT DISULFID 154 167
 FT DISULFID 175 348
 FT DISULFID 247 252
 FT DISULFID 267 283
 FT DISULFID 396 410
 FT DISULFID 421 449
 FT CARBOHYD 196 196
 FT CARBOHYD 207 207
 FT CARBOHYD 228 228
 FT CARBOHYD 285 285
 FT SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;
 Query Match 39.3%; Score 858.5; DB 1; Length 475;
 Best Local Similarity 37.3%; Pred. No. 9.3e-60;
 Matches 167; Conservative 76; Mismatches 138; Indels 67; Gaps 8;

Db 41 ANSFLEEMKQGNITERECNEERCSKEAREAFEDNEXTEEFPMNIVYDGDCCSPCHYGGQ 100
 Qy 61 CKDQLOSYITFCIPABGRNCETHKDDLI---CVNENGCEBOYCSDHGTGRS--CRGH 115
 Db 101 CKDGLSYTSCLDYOGKNCFE---VIPKYCKINNGCEBOFCISIKRSVKDVCSCST 155
 Qy 116 EGYSLADGVSCPTVEYPCGKI-----PILEKRNASKPGQ----- 151
 Db 156 SGLELADGKQCKSVKRYPCGKVLKRIKRSVLLPTNSNTNATSDDDVDSTNGSILEEYF 215
 Qy 152 -----RIVGKVCPCGCEPMQ-VLLVNGAQLCGTILNTI 186
 Db 216 TTTTSPPTPPRNGSSITDPNVDTRIVGDECPGCGCPMNAVILNKKEFEFCGTTLNED 275
 Qy 187 WVTSAHCEPKIKNNMLNLAIVGEHDLSEHDGDSRRVAQVIIPSTVPGTTNHDIALI 246
 Db 276 FILTAHACINQSK---EIKVYGEVDREKESEHETHTAEKIFVHSKYIAETVNDIALI 332
 Qy 247 RLHPVVLTDHVPVPLCPERTFSERTLAFVRSVLVSGMQLDRGATALELVANVRLM 306
 Db 333 KLKEPFOFSEYVPAFLPADRANEVLMNOKSGMWSGFEREDEAGLSRLVLEVPYVD 392
 Qy 307 TODCLQOSRKRVGDSPIITEYMFCAYSDSKDSCKSGSPHATRYGTYLTVGIYSMCO 366
 Db 393 RSPCKQSTNFA-----ITEMFCAGYETEQKDACGDSGPHVTRKYDTFTVGIYSME 447
 Qy 367 GCATVGHFVYRVVSYIEMLOKLRSE 394
 Db 448 GCARKGKRYVYTKLSRFLRMVRYMROK 475
 RESULT 6
 FA10_HUMAN STANDARD; PRT; 488 AA.
 ID FA10_HUMAN
 AC P00742; Q14340;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_Taxid:9606;
 RN [1]
 RP MEDLINE-91216473; PubMed-1902434;
 RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
 RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
 RL human coagulation factor X.";
 RN Gene 99:291-294(1991).
 RN [2]
 RP MEDLINE-87026600; PubMed-3768336;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RN Biochemistry 25:5098-5102(1986).
 RN [3]
 RP MEDLINE-85216545; PubMed-2582420;
 RA Fung W.R., Hay C.W., McGillivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RL blood coagulation factor X.";
 RN Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [4]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-86221713; PubMed-3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood coagulation factor X

- RT "Isolation and characterization of human factor IX cDNA:
RT Identification of Tag I polymorphism and regional assignment.";
RL Somat. Cell Mol. Genet. 10:465-473(1984).
RN [6]
RX SEQUENCE OF 290-359 FROM N.A.
RX MEDLINE-88127096; PubMed-3340835;
RT Scofield E.S., Koebel D.D., Sarker G., Sommer S.S.;
RT "Genomic amplification with transcript sequencing.";
RL Science 239:491-494(1988).
RN [7]
RP SEQUENCE OF 444-461 FROM N.A.
RX MEDLINE-94054330; PubMed-8236150;
RA de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,
RA Wiesel M.L., Grunbaum L., Gazeave J.-P.;
RT "A deletion located in the 3' non translated part of the factor IX
RT gene responsible for mild haemophilia B.";
RL Thromb. Haemost. 70:370-371(1993).
RN [8]
RP SEQUENCE OF 47-461 (VARIANT NAGOVA).
RX MEDLINE-90078229; PubMed-2592373;
RA Suenhiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
RA Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell
RT chymase.";
RL J. Biol. Chem. 264:21257-21265(1989).
RN [9]
RP HYDROXYLATION OF ASP-110.
RX MEDLINE-83308813; PubMed-6688526;
RA McMullen B.A., Fujikawa K., Kistiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [10]
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE-78194509; PubMed-659613;
RT di Scipio R.G., Kunitachi K., Davie E.W.;
RT "Activation of human factor IX (Christmas factor).";
RL J. Clin. Invest. 61:1528-1538(1978).
RN [11]
RP CALCULUM-BINDING DATA.
RX MEDLINE-84185715; PubMed-6425296;
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RT "Derivatives of blood coagulation factor IX contain a high affinity
RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";
RL J. Biol. Chem. 259:5698-5704(1984).
RN [12]
RP ERRATUM.
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
RL J. Biol. Chem. 260:2383-2383(1985).
RN [13]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE-86189947; PubMed-3009023;
RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
RT "Defective propeptide processing of blood clotting factor IX caused
RT by mutation of arginine to glutamine at position -4.";
RL Cell 45:343-348(1986).
RN [14]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE-90062160; PubMed-2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein 2 and bovine protein 2.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [15]
RP STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE-91344709; PubMed-2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein 2.";
RN
- RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [16]
RP STRUCTURE OF CARBOHYDRATE ON SER-107.
RX MEDLINE-92388094; PubMed-1517205;
RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
RT serine 61 through the fucose residue.";
RL J. Biol. Chem. 267:17520-17525(1992).
RN [17]
RP PHOSPHORYLATION OF SER-114.
RA Harris R.O., Pape D.I., Tyuong L., Smith K.J.;
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";
RL (in) Abstracts of xith international conference on methods in protein
RL structure analysis, pp.50-50, Anney (1996).
RN [18]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE-20573597; PubMed-11133752;
RA Arruda V.R., Hagstrom J.N., Delich J., Helman-Patterson T.,
RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
RT Larson P.J., High K.A.;
RT "Posttranslational modifications of recombinant myotube-synthesized
RT human factor IX.";
RL Blood 97:130-138(2001).
RN [19]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-95229607; PubMed-7713897;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
RT binding region of factor IX by two-dimensional NMR spectroscopy.";
RL J. Biol. Chem. 270:7980-7987(1995).
RN [20]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-96032604; PubMed-7547952;
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
RT domain of factor IX.";
RL Biochemistry 34:12126-12137(1995).
RN [21]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-96279169; PubMed-8663165;
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
RA Furie B.;
RT "Identification of the phospholipid binding site in the vitamin K-
RT dependent blood coagulation protein factor IX.";
RL J. Biol. Chem. 271:16227-16236(1996).
RN [22]
RP STRUCTURE BY NMR OF 47-93.
RX MEDLINE-97199336; PubMed-9047312;
RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
RA Smith H., Hiskey R.G., Pedersen L.G.;
RT "Refinement of the NMR solution structure of the
RT gamma-carboxyglutamic acid domain of coagulation factor IX using
RT molecular dynamics simulation with initial Ca2+ positions determined
RT by a genetic algorithm.";
RL Biochemistry 36:2132-2138(1997).
RN [23]
RP STRUCTURE BY NMR OF 91-133.
RX MEDLINE-91308127; PubMed-1854745;
RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;
RT "Sequence-specific 1H NMR assignments, secondary structure, and
RT location of the calcium binding site in the first epidermal growth
RT factor like domain of blood coagulation factor IX.";
RL Biochemistry 30:7402-7409(1991).
RN [24]
RP STRUCTURE BY NMR OF 92-130.
RX MEDLINE-93284090; PubMed-1304885;
RA Barton M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;
RT "The three-dimensional structure of the first EGF-like module of
RT human factor IX: comparison with EGF and TGF-alpha.";
RL Protein Sci. 1:81-90(1992).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.

FT	MOD_RES	72	72	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	75	75	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	79	79	GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	103	103	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	274	274	CHARGE RELAY SYSTEM.
FT	ACT_SITE	320	320	CHARGE RELAY SYSTEM.
FT	ACT_SITE	417	417	CHARGE RELAY SYSTEM.
FT	DISULEID	90	101	BY SIMILARITY.
FT	DISULEID	95	110	BY SIMILARITY.
FT	DISULEID	112	121	BY SIMILARITY.
FT	DISULEID	129	140	BY SIMILARITY.
FT	DISULEID	136	149	BY SIMILARITY.
FT	DISULEID	151	164	BY SIMILARITY.
FT	DISULEID	172	340	INTERCHAIN (BY SIMILARITY).
FT	DISULEID	239	244	BY SIMILARITY.
FT	DISULEID	259	275	BY SIMILARITY.
FT	DISULEID	388	402	BY SIMILARITY.
FT	DISULEID	413	441	BY SIMILARITY.
FT	CARBOHYD	61	61	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	187	187	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	490 AA;	53965 MM;	3A39F8A65AF2A6D11 CRC64;	

Query Match	38.6%	Score 843.5	DB 1	Length 450
Best Local Similarity	37.9%	Pred. NO. 1.4e-58		
Matches 168	Conservative 79	Mismatches 137	Indels 59	Gaps 9

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OY      1 ANNELXXLRFGSLRXKCKKXKXOCSPXXARXITRKDAXRRLFLFISYSDGQOCASSPQONCGS 60
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      41 ANSFLEELKKNGLNRECEMEENCSYEELAEVEDEKKTNEFNKKYVDGDCESHPCONGT 100
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      61 CKDQLOSYICFCLPAFEGRNCE--THAADDOLICVENNGCEQOYCSDHGTGKSCRCHEG 118
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      101 CKDGLGMYTSCVEGEGEGDOCEPYTR---LCSLDNGCQGFCKEENSV-LCSCASGY 155
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      119 SLIADVSCPTPYEYPCGKIPILEKR-----NASK--PQG----- 151
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      156 TLADNGSKSISTELFCGKAYTLGMRKSPATNSSEGEAPEADPEQODDGNLTATENPNL 215
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      152 -----RIVGKYCPKKECPQVLL--VNGQLCGGTLINTIVYSAHC 194
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      216 LDSPEPPEDSSIVRIYVGQDCRODECCRMALLVNEENGFCGGTILSEHYHTAAHC 275
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      195 FDKIKMNRNLIAVLGEHDLSEHDGDECSRVAQYIIPSTYPGTTNHDIALLRLHQPYVL 254
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      276 LHKAKRFK---VAVGCRDTEHEGENEETHVEYVVKNNRFKETYDPDIAVLRLKTPITF 332
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      255 TDHVYVRLCLPERFESBETLAFVRESLYSGNGOLDRGATALEMLVNLVPLMTODCLOOS 314
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      333 RRVAVAPACLOKMAWSESTLMAOQTGIVSGFGRHEMRSLSTLLKMLEVPYVDRNSCKRSS 392
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      315 RRVGDSPNITEYVFCAGYSDGSKDCSGDGGSPATHYRGTWITGLTYSMGCGATVHF 374
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      393 -----SFITQNNFCAGYDARPDACGGDSGGPRVTFRDYTFYTGIVSMEGCARKGK 447
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      375 GYVTRYSOYIEMLQKLMRSEPP 397
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      448 GYVTKYSNFLKTEKSMRAAVP 470
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 10			
FEFA10_BOVIN	STANDARD;	PRT;	492 AA.
FA10_BOVIN			
P00743;			
21-JUL-1986 (Rel. 01, Created)			
13-AUG-1987 (Rel. 05, Last sequence update)			
15-JUN-2002 (Rel. 41, Last annotation update)			
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).			
F10.			
Bos taurus (Bovine) .			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.V., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RL moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor XIa (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]

[illegible]


```

Db 46 GNLRECIETERCSEEAEREVEENTETETFEWKQYVDGQCESNCLNGIGKIDKDISSEEC 105
Qy 71 FCLPFAFGNRCNETHKDDQLICVNGGCEOCSDHTGKSCREHSGYSLADGVSCTPT 130
Db 106 WCVGFGFGRNCEL----DATCNINNGKRCOKPCNKPNNKYCSCTEGTYLAEDKSCPT 161
Qy 131 VEPFGCKRPT-----LEARNASKP 149
Db 162 VPFCGRASISYSKKTITRAETVPSNMDYENSTFAVITODDITDGLNNVTSESESLND 221
Qy 150 OGRVGVKVCPCPKGCPQVILLNGAQLCGTLLNTIMVSAHCF---DKIKMRLIA 206
Db 222 FTRVGVGNKPKGQIPWQVILNGEIEAFCCGAILNEKWIYTAHCLPKGKIE-----V 275
Qy 207 VLGEHDLSEHDGDSQSRVAQVILIPSYVPGTNN---HDALLRLHQPVLVTDHVPCL 263
Db 276 VAEKYNIDKKEDEDQRNVRT--IPHQYNATINKYSHDIALLELDPILINSVYPICV 334
Qy 264 PERTFSERTLAFAVRF--SLVSGNGQLDRGATALALMLVNLVPRMLQDCLQOSRKVGDSP 331
Db 335 ANR---EYTNIFLKFSGYVSGMGKVPENKRHMSILOLVNPLVDATCLR-----ST 384
Qy 322 NITEY--MCCAGISDSKSDCKSDSGPHATYRGTYLTGIVSGGCATVGFYGYTR 379
Db 385 TETTYNNMFCAGYREGKDSCEGDSGPHVTEGTSFLGLISMGECMKRGKGYTR 444
Qy 380 VSOYIEMLOK 389
Db 445 VSRVYMWIKE 454

RESULT 12
FA9_CANFA STANDARD; PRT; 452 AA.
ID FA9_CANFA
AC P19540;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN 11]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=90311364; PubMed=2367529;
RA Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;
RT "Phenotypic correction of factor IX deficiency in skin fibroblasts of
RL hemophilic dogs.",
RL Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990)..
RN 12]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89323338; PubMed=2752110;
RX Evans J.P., Weitzke H.H., Ware J.L., Stafford D.W., High K.A.;
RT "Molecular cloning of a cDNA encoding canine factor IX.",
RL Blood 74:207-212(1989).
RN 13]
RP VARIANT HEMOPHILIA B GLD-418.
RX MEDLINE=90099303; PubMed=2481310;
RX Evans J.P., Brinkhous K.M., Brayer G.D., Relsner H.M., High K.A.;
RT "Canine hemophilia B resulting from a point mutation with unusual
RL consequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).
CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
CC IONS, PHOSPHOLIPIDS, AND FACTOR VIII.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-I-Ile bond in factor X to
CC form factor Xa.

```


Query Match	37.5%	Score 821	DB 1	Length 452
Best Local Similarity	39.5%	Pred. No	7.4e-57	
Matches 163	Conservative	67	Mismatches 133	Indels 50
			Gaps	10

RESULT 13	STANDARD;	PRT;	459 AA.
PRTC_PIG			
AC	PRTC_PIG		
ID	09GILP?		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	15-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Vitamin K dependent protein C precursor (PC 3.4.21.69)		
DE	Antithrombin IIIA (Anticoagulant protein C) (Blood coagulation factor XIV).		
PROC.			
DN			

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RT Kim H.K.W.;
RT "Porcine protein V: cDNA cloning, gene mapping, three-dimensional
protein modeling of membrane binding sites and comparative anatomy of
domains".
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -I- FUNCTION: Protein C is a vitamin K-dependent serine protease that
regulates blood coagulation by inactivating factors Va and VIII
in the presence of calcium ions and phospholipids.
CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
and VIII.
CC -I- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
into a light chain and a heavy chain held together by a disulfide
bond. The enzyme is then activated by thrombin, which cleaves a
tetradecapeptide from the amino end of the heavy chain; this
reaction, which occurs at the surface of endothelial cells, is
strongly promoted by thrombomodulin.
CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
residues allows the modified protein to bind calcium.
CC -I- MISCELLANEOUS: Calcium also binds, with stronger affinity to
another site, beyond the Gla domain. This Gla-independent binding
site is necessary for the recognition of the
thrombin-thrombomodulin complex.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@ebi.ac.uk).

DR EMBL: AF191307; AAC28380.1; -
DR HSP: P04070; IPCU.
DR MEROPS: S01_218; -
DR InterPro: IPRO00152; Asx_hydroxyl.
DR InterPro: IPRO01314; Chymotrypsin.
DR InterPro: IPRO00561; EGF-like.
DR InterPro: IPRO01881; EGF-Ca.
DR InterPro: IPRO02383; GLA_blood.
DR InterPro: IPRO01254; Ser-protease_Try.
DR InterPro: IPRO00294; Ytk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00089; trypsin_1.
DR Pfam: PF00594; gla_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_2.
DR SMART: SM00001; EGF_like_2.
DR SMART: SM00069; GLA_1.
DR SMART: SM00020; trypt_spc_1.
DR PROSITE: PS00010; ASX_HYDROXYL_1.
DR PROSITE: PS00022; EGF_1_1.
DR PROSITE: PS00166; EGF_2_2.
DR PROSITE: PS00187; EGF_CA_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION_1.
DR PROSITE: PS50240; TRYPSIN_DOM_1.
DR PROSITE: PS00134; TRYPsin_HIS_1.
DR PROSITE: PS00135; TRYPsin_SER_1.
KM Gamma-carboxyglutamic acid; Calcium binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.

```

FT SIGNAL 1 18 BY SIMILARITY.
FT PROPER 19 41 BY SIMILARITY.
FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY
FT CHAIN 199 459 SIMILARITY).
FT CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY
FT CHAIN 199 459 SIMILARITY).
FT PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 213 214 CLEAVAGE (BY THROMBIN) (BY
FT SITE 213 214 SIMILARITY).
FT DOMAIN 96 131 EGF-LIKE 1.
FT DOMAIN 135 175 EGF-LIKE 2.
FT DOMAIN 214 459 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 48 48 SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 55 55 SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 57 57 SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 60 60 SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 61 61 SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 66 66 SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 67 67 SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 SIMILARITY).
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 235 235 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 131 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 36.0%; Score 786.5; DB 1; Length 459;
Best Local Similarity 39.4%; Pred. No. 3.7e-54;
Matches 166; Conservative 65; Mismatches 151; Indels 39; Gaps 11;

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DB 277 KNEVDIDIEFLVHPNVTSTSDNDIALRLAPATFSOTIVPICPDLSERELTRVG 336
QY 277 RESVSGMQLDORGTALEMLWN---VPRLTQOCLQSRVGVSDPNTYEFACAGS 333
DB 337 QETVTVGMKYSRSE--AKTRSPFLNFIKYPVAPVAPNECVQAMN-----KISEMMLCAGIL 389
QY 334 DSKSDCKDSDGSGPHATRYGTWYLTGIVSMGCGATVGHFGVYTVSVOYIEWLQRLMRS 393
DB 390 GDSRDACEGSDSGPMAVSFRGTWFLVGLVSWEGCCRLNNYGVYTVSRLDMTHIGHIRN 449
QY 394 E 394
DB 450 E 450

RESULT 14
PRTC_RAT STANDARD; PRT; 461 AA.
AC P31394;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
DE PROC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92329550; PubMed=1627650;
RX Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -I- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADCAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -I- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -I- MISCELLANEOUS: CALCIUM ALSO BINDS. WITH STRONG AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC
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CC or send an email to license@sdb.ch).
CC
CC EMBL; X64336; CAA45617.1;
CC PIR; S18994; S18994.
CC PIR; S24312; S24312.
CC HSRP; P04070; 1PCU.
CC MEROPS; S01.218;
CC InterPro; IPR000152; Asx_hydroxyl.

```

DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser-protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00594; gla; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_1like; 1.
 DR SMART: SM00068; GLA; 1.
 DR SMART: SM00020; tryp-Spc; 1.
 DR PROSITE: PS0010; ASX_HYDROXYL; 1.
 DR PROSITE: PS0186; EGF_2; 2.
 DR PROSITE: PS0186; EGF_1; 1.
 DR PROSITE: PS0187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Blood coagulation: Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; signal.
 FT SIGNAL 1 32
 FT PROPEP 1 32
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61
 FT MOD_RES 66 66
 FT MOD_RES 67 67
 FT MOD_RES 70 70
 FT MOD_RES 70 70
 FT MOD_RES 112 112
 FT ACT_SITE 254 254
 FT ACT_SITE 300 300
 FT ACT_SITE 402 402
 FT ACT_SITE 58 63
 FT ACT_SITE 91 110
 FT ACT_SITE 100 105
 FT ACT_SITE 104 110
 FT ACT_SITE 121 130
 FT ACT_SITE 139 150
 FT ACT_SITE 146 159
 FT ACT_SITE 161 174
 FT ACT_SITE 182 320
 FT ACT_SITE 239 255
 FT ACT_SITE 373 387
 FT ACT_SITE 398 426
 FT ACT_SITE 215 215
 FT CARBOHYD 291 291
 FT CARBOHYD 355 355
 FT CARBOHYD 461 AA; 51912 MW; 844CF93664EDACD5 CRC64;
 FT SEQUENCE

Query Match 35.4%; Score 775; DB 1; Length 461;
 Best Local Similarity 37.7%; Pred. No. 2.9e-53;
 Matches 164; Conservative 67; Mismatches 156; Indels 48; Gaps 11;
 1 ANAFLXLRPGLRXXKXKXQCSFXAXRXIFKDAKTKLFWISYSDGDCAS-----52
 42 ANSFLFEVRAGSLERCMEDICDFEAOEIFQVDETLAFWIRYFGDCCSTPPLDHOD 101
 53 SPQNGSCSKDQLOSTICFLPAFEGRNCEETHKDDQLICVNGGCEGYCSHTGTGRSC 112
 102 SPCCGHGTCTIDIGLGFSCGCDKMGEGRCFCQEGFQ-DCRVKNGCGYHLCLETRGR-C 159
 113 RCHEGYSLADGVSCPTVEYPCGKIPLEKRNASRPG-----RIVG 156
 160 RCAPGTELDADHHCPTVNFPGK---LWKRTDKRKRFKRDIDPEDELELGPRIYVG 216
 157 KYCPKGECPMVLVLLVNGAQL-CGGTLNTIIVWSAAGCFDKIKMNRNLIAVGEHDLSE 215
 217 TLTQGDSPMAIILDSKKKACGGVLIHTSWLTAHGLESSK---KLTVALGEIDLNR 273
 216 HGGDESRNVAQYIIPSTYVPGTTHDIALRLHQPVLTDHVPCLCPERTFSERTIAF 275
 274 RDPWEIDLDIKETLVHPNTRNSNDIALLRLSQPATLSTKIYVPICLPNSGLAQLSQA 333
 276 VRFSTVSGMGQLD-----RGATALELVAVNPRIMTQDCQOSRKVGSNITETVFC 329
 334 GGEIVYTGNGYSDKVKDGRNRRTFL-LTFIRIPLAARDCKQVNNV-----VSENMIC 387
 330 AGYSDGSKDSCGSGPNAHYRGTWYLTGIYVSGGCAVGVHGFYRVSQYIEMLOK 389
 388 AGIIGTRDAGCGDSGGPMVVFRRGTWFLVGLVSGEGCHLNNYGVITTKVSYLKIHS 447
 390 LMRSEPRVLLRAP 404
 448 YIGER---DVSLKSP 459
 DB
 RESULT 15
 PRTC_MOUSE
 ID PRTC_MOUSE STANDARD; PRT; 461 AA.
 AC P33587; O35498;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
 DE PROC.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=92316697; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=128/SVJ;
 RA MEDLINE=98152576; PubMed=9493582;
 RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding
 RT anticoagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 RN [3]
 RP SEQUENCE OF 274-434 FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=94318474; PubMed=8043441;

RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nino Y.;
 RT "A comparative study of partial primary structures of the catalytic
 RL region of mammalian protein C.";
 CC Br. J. Haematol. 86:590-600(1994).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIa.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sdb.ch).
 CC -----
 DR EMBL: D10445; BAA01235.1;
 DR EMBL: AF034569; AAC3795.1;
 DR EMBL: D43755; BAA07812.1;
 DR PIR: JX0210; JX0210.
 DR HSSP: P04070; 1PCU.
 DR MEROPS: S01.218;
 DR MGD: MGI:97771; PROC.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR000294; VltK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00089; trypsin_1.
 DR Pfam: PF00584; glia_1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0001; GLABLOOD.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_Spe; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT SIGNAL 1 33
 FT PROPEP 34 41
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).

QY	DOMAIN	96	131	EGF-LIKE 1.
FT	DOMAIN	135	175	EGF-LIKE 2.
FT	DOMAIN	213	461	SERINE PROTEASE.
FT	MOD_RES	47	47	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	48	48	(BY SIMILARITY).
FT	MOD_RES	48	48	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	55	55	(BY SIMILARITY).
FT	MOD_RES	57	57	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	60	60	(BY SIMILARITY).
FT	MOD_RES	61	61	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	66	66	(BY SIMILARITY).
FT	MOD_RES	67	67	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	70	70	(BY SIMILARITY).
FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	112	112	(BY SIMILARITY).
FT	MOD_RES	253	253	HYDROXYLATION (BY SIMILARITY).
FT	MOD_RES	299	299	CHARGE RELAY SYSTEM.
FT	MOD_RES	402	402	CHARGE RELAY SYSTEM.
FT	MOD_RES	58	58	CHARGE RELAY SYSTEM.
FT	MOD_RES	91	110	BY SIMILARITY.
FT	MOD_RES	100	105	BY SIMILARITY.
FT	MOD_RES	104	119	BY SIMILARITY.
FT	MOD_RES	121	130	BY SIMILARITY.
FT	MOD_RES	139	150	BY SIMILARITY.
FT	MOD_RES	146	159	BY SIMILARITY.
FT	MOD_RES	161	174	BY SIMILARITY.
FT	MOD_RES	182	319	INTERCHAIN (BY SIMILARITY).
FT	MOD_RES	238	254	BY SIMILARITY.
FT	MOD_RES	373	387	BY SIMILARITY.
FT	MOD_RES	398	426	BY SIMILARITY.
FT	MOD_RES	214	214	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES	230	230	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES	328	328	MISSING (IN REF. 2).
FT	MOD_RES	393	393	N -> D (IN REF. 2).
SO	SEQUENCE	461 AA:	51945 MW:	53FAAD085B194D6E CRC64:

Query Match 35.2% Score 769; DB 1; Length 461;
 Best Local Similarity 36.9%; Pred. No. 8; 5e-53;
 Matches 159; Conservative 80; Mismatches 150; Indels 42; Gaps 12;

QY	1	ANAFLEXLRPGSLXKXKXOCSPXAXXIFRDAARTLFWYISYDGGQAS-----	52
DB	42	ANSFLEENRPPSLERECEMEICDFEAOEITQNVEDTLAFWIKYFDGQCSAPPLDHOC	101
QY	53	SPCNGSGCKDOLQSYICFCLPAFEGRCNCFTHKQDLQCVENGGCEQCSQHTKSC	112
DB	102	SPCGHGTCIDIGISFSCSKDCKGKGCQDELPRQDQRVN-NGSCLHYCEESNGRR-C	159
QY	113	RCHBGYSILADGVSCFPEVVEYPCGKIP--LEKRNASK-----POGRYGGKCP	160
DB	160	ACARGYELADHMKCKSTVNEPCGKLGMIKKRILKRDLDLEDELPDRIVNGITLK	219
QY	161	KGECPMOVLILLVNGAOL-CGGTLLNTIIVVSAANCFCIKKRNRLIANVLGEHDSHGD	219
DB	220	QGDSPWQITLDSKKKLACGGVLLHTSVLLTAAC--VEGTRKLTVLAGEVDLRRRDHW	276
QY	220	EOSRRVAVIIPSTYVGTNHDIALRLHPVVLTDHVPCLPERFESRTLAFLV-RF	278
DB	277	ELDDDIKELVHPYTTSSSDNDLRLAPALSLKTIYVICLPNNGLAQDELTOAGOE	336
QY	279	SLVSGWQLD-----RGATALELVANLPRMTODLOQSRKVGDSPIITEYFCAGY	332
DB	337	TVVYGWGYOSDRIKDGRNRNTEFI-LTFIRIPLVARNCEVEMKNV-----VSEMLCAGI	390
QY	333	SDGSKDCKDSCGPHATHTHRTGYVLTGIYSWGCGCATVGHFGYTVRSOTIEWLQKLMR	392

Db 391 IGNTRDACDGDGSGPMVVFRRGTWFLVGLVSMGCGHTNNYGIYTKVGSYLKWIHSYIG 450
OY 393 SEPRGVLLRA 403
Db 451 EK--GVSLKS 458

Search completed: July 1, 2003, 17:52:16
Job time : 25 secs